Construction of the HIV-2/SIV alignments

Classification of the sequences

Classification of HIV-2 is straightforward, as the subtype classification of this virus is more or less standardized. Classification of the SIVs is more complicated. There are two major groups of SIV sequences, SIV-agm and SIV-mac (clustering closely with HIV-1). These two main groups are represented in separate alignments in this Compendium. However, some SIV sequences fall far outside these clusters. In some cases (notably SIV-mnd and the new SIVI') hoest sequence), we have decided not to include the sequences in any alignment because they are so diverged that including them would require a large number of gaps, making the alignment very hard to read. The new SIVrcm (red-capped mangabey) sequence that was published this year (1) poses a different problem: it appears to be a recombinant, with the Pol gene clustering loosely with the SIV-cpz's, and the Gag region clustering between the AGM and that clustering loosely with the SIV-cpz's, and the Gag region clustering between the AGM and that clustering loosely with the SIV-cpz's, and the Gag region clustering between the AGM and MAC/HIV-2 clustering loosely with the SIV-cpz's, and the Gag region clustering between the AGM and that clustering loosely was longer than that clustering with the SIVcpz's. Because the new Drill Monkey SIV pol gene resembles SIVrcm most closely (2), this sequence was also added to the HIV-2. SIVmac alignment.

In the HIV-2/SIV alignment, the classification of the SIVsm and SIVmac sequences into SIVmac-SD is probably a simplification. 'SD' stands for 'Simian subtype D'. This classification is based on the fact that they cluster together with the only HIV-2 subtype D isolate known, FO784. For more information on HIV-2 and SIV phylogeny, see (3).

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